

IN THE CLAIMS:

Please amend the claims as follows.

Claim 1 (Previously Presented): An isolated rpoB nucleic acid fragment of a molecule consisting of a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 8, 9 and 10, wherein said fragment consists of at least about 100 contiguous bases of said sequence.

Claim 2 (Previously Presented): An isolated nucleic acid molecule consisting of a rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9 and 10.

Claim 3 (Previously Presented): A probe which is the complement of a rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10.

Claim 4 (Previously Presented): A method of classifying a mycobacteria, comprising
providing a sample comprising a mycobacterial rpoB target nucleic acid from a mycobacteria;
determining the sequence of a segment of at least 50 contiguous bases from the target nucleic acid;
comparing the determined sequence to at least one sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10; and
classifying the mycobacteria from the extent of similarity of the compared sequences.

Claim 5 (Original): The method of claim 4, wherein at least 100 contiguous bases are determined from the target nucleic acid.

Claim 6 (Previously Presented): The method of claim 4, wherein the determined sequence is compared with at least nine sequences selected from the group consisting SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10.

Claim 7 (Currently Amended): A method of classifying a mycobacteria, comprising

providing a sample comprising a mycobacterial rpoB target nucleic acid;
determining the identity of one or more bases in the target sequence at one or more positions corresponding to one or more bases in a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10, wherein the one or more bases of the sequence selected from the group consisting of SEQ ID NOS: NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10 differ from the corresponding one or more bases in SEQ ID NO: NO: 1 when the sequences are maximally aligned, the identity of the one or more bases characterizing the species of mycobacteria that is present in the sample;
comparing the identified one or more bases in the target sequence to at least one sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10; and
classifying the mycobacteria from the extent of similarity between the one or more bases identified in the target sequence and the corresponding one or more bases in the compared sequences.

Claim 8 (Previously Presented): The method of claim 7, wherein the identity of at least 10 bases in the target nucleic acid at positions corresponding to the one or more bases in the sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10 is determined.

Claim 9 (Previously Presented): The method of claim 8, wherein the identity of at least 20 bases in the target sequence at positions corresponding to the one or more bases in the sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10 is determined.

Claim 10 (Previously Presented): The method of claim 9, further comprising comparing the at least 20 determined bases with at least 20 bases occupying corresponding positions in each of at least nine sequences selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6, 7, 8, 9, and 10.

Claim 11 (Previously Presented): A polynucleotide probe or primer that hybridizes under stringent hybridization conditions to a mycobacterial rpoB sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6 and 9 or its complement without hybridizing to

the *M. tuberculosis* sequence of SEQ ID NO: 1 or its complement, wherein said stringent hybridization conditions comprise 5 X SSPE and a temperature of 25-30°C.

Claim 12 (Previously Presented): The polynucleotide of claim 11 that is a probe.

Claim 13 (Previously Presented): The polynucleotide of claim 12, wherein a central position of the probe aligns with one or more bases of a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6 and 9 which differ from the corresponding one or more bases in SEQ ID NO: 1 when the sequences are maximally aligned.

Claim 14 (Previously Presented): The sequence-specific polynucleotide of claim 11 that is a primer.

Claim 15 (Previously Presented): The polynucleotide of claim 14, wherein the 3' end of the primer aligns with one or more bases of a sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6 and 9 which differ from the corresponding one or more bases in SEQ ID NO: 1 when the sequences are maximally aligned.

Claim 16 (Previously Presented): The polynucleotide of claim 11 that hybridizes under stringent hybridization conditions to at least 100 contiguous bases of a mycobacterial *rpoB* sequence selected from the group consisting of SEQ ID NOS: 2, 3, 4, 5, 6 and 9 or its complement without hybridizing to the *M. tuberculosis* sequence of SEQ ID NO:1 or its complement.

Claim 17 (Currently Amended): A polynucleotide probe or primer that hybridizes under stringent hybridization conditions to at least 100 contiguous bases of a mycobacterial *rpoB* sequence selected from the group consisting of SEQ ID NOS: 8 and 10 or its complement without hybridizing to the *M. tuberculosis* sequence of SEQ ID NO:1 or its complement, wherein said stringent hybridization conditions comprise 5 x SSPE and a temperature of 25-30°C.

Claim 18 (Previously Presented): The polynucleotide of claim 17, wherein the polynucleotide is a probe, and wherein a central position of the probe aligns with one or more

bases of a sequence selected from the group consisting of SEQ ID NOS: 8 and 10 which differ from the corresponding one or more bases in SEQ ID NO: 1 when the sequences are maximally aligned.

Claim 19 (Previously Presented): The polynucleotide of claim 17, wherein the polynucleotide is a primer, and wherein the 3' end of the primer aligns with one or more bases of a sequence selected from the group consisting of SEQ ID NOS: 8 and 10 which differ from the corresponding one or more bases in SEQ ID NO: 1 when the sequences are maximally aligned.